

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/677,977A  
Source: 1FW/6  
Date Processed by STIC: 9/30/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

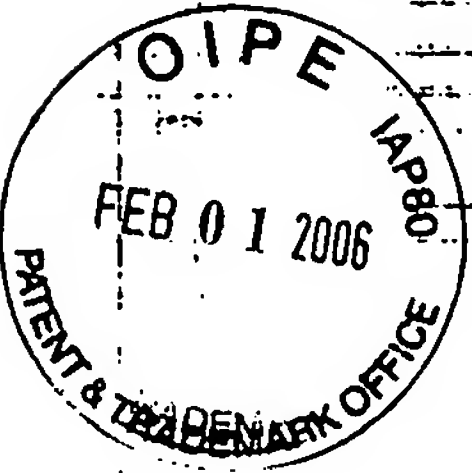
<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

BEST AVAILABLE COPY



## Raw Sequence Listing Error Summary

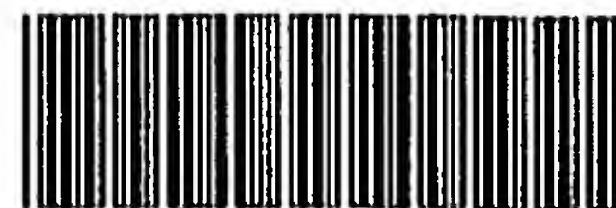
### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/677,977A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor after creating it. Please adjust your right margin to 3. this will  
                              prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers:  
     Numbering                use space characters, instead.
  
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                              ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length       Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                              each n or Xaa can only represent a single residue. Please present the maximum number of each  
                              residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                    sequences(s)             . Normally, PatentIn would automatically generate this section from the  
                              previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                              the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                              Artificial or Unknown sequences.
  
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                              (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                              (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                              This sequence is intentionally skipped  
  
                              Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                              <400> sequence id number  
                              000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                              In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                              is Artificial Sequence
  
- 11      Use of <220>        Sequence(s)              missing the <220> "Feature" and associated numeric identifiers and responses.  
                              Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                              "Unknown." Please explain source of genetic material in <220> to <223> section.  
                              (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                              listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa       "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 09/30/2005

PATENT APPLICATION: US/10/677,977A

TIME: 12:09:27

Input Set : A:\25840-501.txt

Output Set: N:\CRF4\09302005\J677977A.raw

3 <110> APPLICANT: Nguyen, Jack  
4 Thanos, Chris  
5 Waugh Ruggles, Sandra  
6 Craik, Charles S.  
8 <120> TITLE OF INVENTION: METHODS OF GENERATING AND SCREENING FOR PROTEASES WITH  
ALTERED  
9 SPECIFICITY  
11 <130> FILE REFERENCE: 25840-501  
13 <140> CURRENT APPLICATION NUMBER: 10/677,977A  
14 <141> CURRENT FILING DATE: 2003-10-02  
16 <150> PRIOR APPLICATION NUMBER: 60/425,388  
17 <151> PRIOR FILING DATE: 2002-10-02  
19 <160> NUMBER OF SEQ ID NOS: 20  
21 <170> SOFTWARE: PatentIn version 3.3  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 277  
25 <212> TYPE: PRT  
26 <213> ORGANISM: Homo sapiens  
28 <400> SEQUENCE: 1  
30 Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu  
31 1 5 10 15  
34 Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser  
35 20 25 30  
38 Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile  
39 35 40 45  
42 Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg  
43 50 55 60  
46 Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn  
47 65 70 75 80  
50 Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile  
51 85 90 95  
54 Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser  
55 100 105 110  
58 Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe  
59 115 120 125  
62 Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg  
63 130 135 140  
66 Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile  
67 145 150 155 160  
70 Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser  
71 165 170 175  
74 Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Asp Ala Asp  
75 180 185 190  
78 Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn

Does Not Comply  
Affected Diskette Needs  
pg 2-3

## RAW SEQUENCE LISTING

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Input Set : A:\25840-501.txt

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79                    195                    200                    205  
82 Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys  
83           210                    215                    220  
86 Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
87 225                    230                    235                    240  
90 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
91                    245                    250                    255  
94 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu  
95                    260                    265                    270

98 Leu Tyr Phe Tyr His

99                    275

102 &lt;210&gt; SEQ ID NO: 2

103 &lt;211&gt; LENGTH: 6

104 &lt;212&gt; TYPE: PRT

105 &lt;213&gt; ORGANISM: Homo sapiens

107 &lt;400&gt; SEQUENCE: 2

109 Phe Ser Phe Asp Ala Thr

110 1                    5

113 &lt;210&gt; SEQ ID NO: 3

114 &lt;211&gt; LENGTH: 42

115 &lt;212&gt; TYPE: DNA

116 &lt;213&gt; ORGANISM: Artificial Sequence

118 &lt;220&gt; FEATURE:

119 &lt;223&gt; OTHER INFORMATION: Granzyme B Mutation Forward Primer

121 &lt;400&gt; SEQUENCE: 3

122 ccagcgtata attctaagac agcctccaat gacatcatgc tg

42

125 &lt;210&gt; SEQ ID NO: 4

126 &lt;211&gt; LENGTH: 6

127 &lt;212&gt; TYPE: PRT

128 &lt;213&gt; ORGANISM: Homo sapiens

130 &lt;400&gt; SEQUENCE: 4

132 Ile Glu Thr Asp Ser Gly

133 1                    5

136 &lt;210&gt; SEQ ID NO: 5

137 &lt;211&gt; LENGTH: 42

138 &lt;212&gt; TYPE: DNA

139 &lt;213&gt; ORGANISM: Artificial Sequence

141 &lt;220&gt; FEATURE:

142 &lt;223&gt; OTHER INFORMATION: Granzyme B Mutation Reverse Primer

144 &lt;400&gt; SEQUENCE: 5

145 cagcatgatg tcattggagg ctgtcttaga attatacgct gg

42

148 &lt;210&gt; SEQ ID NO: 6

149 &lt;211&gt; LENGTH: 6

150 &lt;212&gt; TYPE: PRT

151 &lt;213&gt; ORGANISM: Homo sapiens

154 &lt;220&gt; FEATURE:

155 &lt;221&gt; NAME/KEY: Variant

156 &lt;222&gt; LOCATION: (1)..(1)

157 &lt;223&gt; OTHER INFORMATION: Wherein Xaa is an N-acetyl group.

Xaa can only represent a  
single amino acid,  
nothing else

(see item 13  
on Error Summary Sheet)

## RAW SEQUENCE LISTING

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Input Set : A:\25840-501.txt

Output Set: N:\CRF4\09302005\J677977A.raw

159 <220> FEATURE:  
160 <221> NAME/KEY: Variant  
161 <222> LOCATION: (6)..(6)  
162 <223> OTHER INFORMATION: *same env* Wherein Xaa is a 7-amino-4-methylcoumarin group.  
164 <400> SEQUENCE: 6  
W--> 166 Xaa Ile Glu Pro Asp Xaa  
167 1 5  
170 <210> SEQ ID NO: 7  
171 <211> LENGTH: 4  
172 <212> TYPE: PRT  
173 <213> ORGANISM: Homo sapiens  
175 <400> SEQUENCE: 7  
177 Ala Glu Ala Lys  
178 1  
181 <210> SEQ ID NO: 8  
182 <211> LENGTH: 4  
183 <212> TYPE: PRT  
184 <213> ORGANISM: Homo sapiens  
186 <400> SEQUENCE: 8  
188 Glu Asn Val Lys  
189 1  
192 <210> SEQ ID NO: 9  
193 <211> LENGTH: 4  
194 <212> TYPE: PRT  
195 <213> ORGANISM: Homo sapiens  
197 <400> SEQUENCE: 9  
199 Gly Thr Glu Asp  
200 1  
203 <210> SEQ ID NO: 10  
204 <211> LENGTH: 4  
205 <212> TYPE: PRT  
206 <213> ORGANISM: Homo sapiens  
208 <400> SEQUENCE: 10  
210 Ser Pro Thr Arg  
211 1  
214 <210> SEQ ID NO: 11  
215 <211> LENGTH: 4  
216 <212> TYPE: PRT  
217 <213> ORGANISM: Homo sapiens  
219 <400> SEQUENCE: 11  
221 Val Ser Thr Arg  
222 1  
225 <210> SEQ ID NO: 12  
226 <211> LENGTH: 4  
227 <212> TYPE: PRT  
228 <213> ORGANISM: Homo sapiens  
230 <400> SEQUENCE: 12  
232 Ser Thr Ser Phe  
233 1



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TIME: 12:09:27

Input Set : A:\25840-501.txt

Output Set: N:\CRF4\09302005\J677977A.raw

236 <210> SEQ ID NO: 13  
237 <211> LENGTH: 4  
238 <212> TYPE: PRT  
239 <213> ORGANISM: Homo sapiens  
241 <400> SEQUENCE: 13  
243 Lys Phe Pro Asp  
244 1  
247 <210> SEQ ID NO: 14  
248 <211> LENGTH: 4  
249 <212> TYPE: PRT  
250 <213> ORGANISM: Homo sapiens  
252 <400> SEQUENCE: 14  
254 Ala Glu Gln Arg  
255 1  
258 <210> SEQ ID NO: 15  
259 <211> LENGTH: 4  
260 <212> TYPE: PRT  
261 <213> ORGANISM: Homo sapiens  
263 <400> SEQUENCE: 15  
265 Lys Tyr Ala Asp  
266 1  
269 <210> SEQ ID NO: 16  
270 <211> LENGTH: 4  
271 <212> TYPE: PRT  
272 <213> ORGANISM: Homo sapiens  
274 <400> SEQUENCE: 16  
276 Asn Gly Pro Lys  
277 1  
280 <210> SEQ ID NO: 17  
281 <211> LENGTH: 4  
282 <212> TYPE: PRT  
283 <213> ORGANISM: Homo sapiens  
285 <400> SEQUENCE: 17  
287 Ser Ser Ala Tyr  
288 1  
291 <210> SEQ ID NO: 18  
292 <211> LENGTH: 4  
293 <212> TYPE: PRT  
294 <213> ORGANISM: Homo sapiens  
296 <400> SEQUENCE: 18  
298 Gly Thr Ser Asp  
299 1  
302 <210> SEQ ID NO: 19  
303 <211> LENGTH: 4  
304 <212> TYPE: PRT  
305 <213> ORGANISM: Homo sapiens  
307 <400> SEQUENCE: 19  
309 Ala Gln Glu Lys  
310 1

RAW SEQUENCE LISTING

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TIME: 12:09:27

Input Set : A:\25840-501.txt

Output Set: N:\CRF4\09302005\J677977A.raw

313 <210> SEQ ID NO: 20  
314 <211> LENGTH: 4  
315 <212> TYPE: PRT  
316 <213> ORGANISM: Homo sapiens  
318 <400> SEQUENCE: 20  
320 Arg Ile Asp Tyr  
321 1

RAW SEQUENCE LISTING ERROR SUMMARY  
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DATE: 09/30/2005  
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Input Set : A:\25840-501.txt  
Output Set: N:\CRF4\09302005\J677977A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 1,6



VERIFICATION SUMMARY

DATE: 09/30/2005

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Input Set : A:\25840-501.txt

Output Set: N:\CRF4\09302005\J677977A.raw

L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0